

RAW SEQUENCE LISTING

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Application Serial Number: 09/485,650
Source: IPW16
Date Processed by STIC: 8/22/05

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IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/485,650

DATE: 08/22/2005
TIME: 08:33:16

Input Set : A:\Cml817.app
Output Set: N:\CRF4\08222005\I485650.raw

3 <110> APPLICANT: Bettiol, Jean-Luc P.
 4 Thoen, Christiaan AJK
 6 <120> TITLE OF INVENTION: Detergent Compositions Comprising a Mannanase and a
 7 Soil Release Polymer
 9 <130> FILE REFERENCE: Mannanase and soil release polymer
 11 <140> CURRENT APPLICATION NUMBER: 09/485,650
C--> 12 <141> CURRENT FILING DATE: 2000-04-05
 14 <150> PRIOR APPLICATION NUMBER: PCT/US98/12027
 15 <151> PRIOR FILING DATE: 1998-06-10
 17 <160> NUMBER OF SEQ ID NOS: 6
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1482
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Bacillus sp.
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 28 ggaataatgg ggattacaac gtccccatca gcagoaagta caggctttt tgTTgatggc 120
 29 aatacgttat atgacgcaaa tgggcagcca tttgtcatga gaggtattaa ccatggacat 180
 30 gcttggata aagacaccgc ttcaacagct attccgtcca ttgcagagca aggcccaac 240
 31 acgattcgta ttgtttatc agatggcggt caatggaaa aagacgacat tgacaccatt 300
 32 cgtgaagtca ttgagcttgc ggagcaaaat aaaatggtgg ctgtcggtga agttcatgtat 360
 33 gccacgggtc gcgattcgcg cagtgattt aatcgagccg ttgattattt gataaaaaatg 420
 34 aaagatgcgc ttatcggtaa agaagatacg gttatttata acattgcaaa cgagtggat 480
 35 gggagttggg atggctcgc ttggccgat ggctatatgg atgtcatttc gaagcttcgc 540
 36 gatgccggct taacacacac cttaatgggt gatgcagcag gatggggca atatccgcaa 600
 37 tctattcatg attacggaca agatgtgtt aatgcagatc cgtaaaaaaaa tacgtatgtc 660
 38 tccatccata tgtatgagta tgctgggtt gatgctaaca ctgttagatc aaatattgtat 720
 39 agagtcatag atcaagacct tgctctcgta ataggtgaat tcggtcatac acataactgtat 780
 40 ggtgatgtt atgaagatac aatccttagt tattctgaag aaactggcac agggtggctc 840
 41 gcttggctt gcaaaggcaa cagtaccgaa tgggactatt tagaccttcc agaagactgg 900
 42 gctggtaaac atttaactga ttggggaaat agaattgtcc acggggccga tggcttacag 960
 43 gaaacctcca aaccatccac cgtatttaca gatgataacg gtggtcaccc tgaaccgcca 1020
 44 actgctacta cttgtatga ctttgaagga agcacacaag ggtggcatgg aagcaacgtg 1080
 45 accgggtggcc cttggccgt aacagaatgg ggtgcttcag gtaactactc tttaaaagcc 1140
 46 gatgtaaatt taacctcaa ttcttcacat gaactgtata gtgaacaaag tcgtaatcta 1200
 47 cacggatact ctcagctaa cgcaaccgtt cgccatgcca attggggaaa tcccggtaat 1260
 48 ggcattaaatg caagacttta cgtaaaaacg ggctctgatt atacatggca tagcggtcct 1320
 49 ttacacgttcaatagtc caactcaggg acaacgtt ctttgattt aaacaacatc 1380
 50 gaaaaatagtc atcatgttag gaaaaataggc gtgcaatttt cagcggcaga taatagcagt 1440
 51 ggtcaactg ctctatacgt tgataacgtt actttaagat ag 1482
 54 <210> SEQ ID NO: 2
 55 <211> LENGTH: 493

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56 <212> TYPE: PRT
 57 <213> ORGANISM: Bacillus sp.
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 63 Ile Ile Ser Val Gly Ile Met Gly Ile Thr Thr Ser Pro Ser Ala Ala
 64 20 25 30
 66 Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly
 67 35 40 45
 69 Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
 70 50 55 60
 72 Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
 73 65 70 75 80
 75 Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
 76 85 90 95
 78 Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
 79 100 105 110
 81 Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
 82 115 120 125
 84 Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
 85 130 135 140
 87 Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
 88 145 150 155 160
 90 Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile
 91 165 170 175
 93 Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala
 94 180 185 190
 96 Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp
 97 195 200 205
 99 Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met
 100 210 215 220
 102 Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp
 103 225 230 235 240
 105 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
 106 245 250 255
 108 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser
 109 260 265 270
 111 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser
 112 275 280 285
 114 Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His
 115 290 295 300
 117 Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln
 118 305 310 315 320
 120 Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His
 121 325 330 335
 123 Pro Glu Pro Pro Thr Ala Thr Leu Tyr Asp Phe Glu Gly Ser Thr
 124 340 345 350
 126 Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr
 127 355 360 365

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129 Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu
130      370          375          380
132 Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu
133 385          390          395          400
135 His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly
136      405          410          415
138 Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser
139      420          425          430
141 Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn
142      435          440          445
144 Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ser His
145 450          455          460
147 His Val Arg Glu Ile Gly Val Gln Phe Ser Ala Ala Asp Asn Ser Ser
148 465          470          475          480
150 Gly Gln Thr Ala Leu Tyr Val Asp Asn Val Thr Leu Arg
151      485          490
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156 <212> TYPE: DNA
157 <213> ORGANISM: Bacillus sp.
159 <400> SEQUENCE: 3
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161 ggaataatgg ggattacaac gtcccccata gcagcaagta caggcttta tggatggc 120
162 aatacgttat atgacgc当地 tggcagcca tttgtcatga gaggtattaa ccatggacat 180
163 gcttggata aagacaccgc ttcaacagct attcctgccca ttgcagagca aggcccaac 240
164 acgattcgta ttgtttatc agatggcggt caatggaaa aagacgacat tgacaccatt 300
165 cgtgaagtca ttgagcttgc ggagaaaaat aaaatggtgg ctgtcgatg agttcatgat 360
166 gccacgggtc gcgattcgcg cagtgattta aatcgagccg ttgattattt gatagaaatg 420
167 aaagatgc当地 ttatcgtaa agaagatacg gttatttata acattgcaaa cgagtggat 480
168 gggagttggg atggctcagc ttggccgat ggctatattt atgtcatcc gaagcttcgc 540
169 gatgccggct taacacacac cttaatggtt gatcagcag gatggggca atatccgcaa 600
170 tctattcatg attacggaca agatgtgtt aatgcagatc cgtaaaaaaaa tacatgttc 660
171 tccatccata tgtatgatgta tgctgggtt gatgctaaca ctgttagatc aaatattgat 720
172 agagtcatag atcaagaccc tgcctcgta ataggtaat tcggcatag acatactgat 780
173 ggtgatgtt atgaagatac aatccttagt tattctgaag aaactggcac agggtggctc 840
174 gcttggtctt ggaaaggcaa cagtaccgaa tgggactatt tagaccttc agaagactgg 900
175 gctggtaaac attaactga ttggggaaat agaattgtcc acggggccga tggcttacag 960
176 gaaacctcca aaccatccac cgtatattaca gatgataacg gtggtcaccc tgaaccgcca 1020
177 actgctacta ctttgatga ctttgaagga agcacacaaag ggtggcatgg aagcaacgtg 1080
178 accgggtggcc cttggccgt aacagaatgg ggtgcttcag gtaactactc tttaaaagcc 1140
179 gatgtaaatt taacctaaa ttcttcacat gaaactgtata gtgaacaaag tcgtaatcta 1200
180 cacggatact ctcagctaa cgcaaccgtt cgccatgccca attggggaaa tcccgtaat 1260
181 ggcataatg caagacttta cgtaaaaacg ggctctgatt atacatggca tagcggtcct 1320
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187 <211> LENGTH: 468
188 <212> TYPE: PRT
189 <213> ORGANISM: Bacillus sp.

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196   20          25           30
198 Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly
199   35          40           45
201 Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
202   50          55           60
204 Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
205   65          70           75           80
207 Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
208   85          90           95
210 Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
211   100         105          110
213 Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
214   115         120          125
216 Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
217   130         135          140
219 Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
220   145         150          155          160
222 Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile
223   165         170          175
225 Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala
226   180         185          190
228 Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp
229   195         200          205
231 Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met
232   210         215          220
234 Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp
235   225         230          235          240
237 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His
238   245         250          255
240 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser
241   260         265          270
243 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser
244   275         280          285
246 Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His
247   290         295          300
249 Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln
250   305         310          315          320
252 Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His
253   325         330          335
255 Pro Glu Pro Pro Thr Ala Thr Thr Leu Tyr Asp Phe Glu Gly Ser Thr
256   340         345          350
258 Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr
259   355         360          365
261 Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu
262   370         375          380

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264 Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu
 265 385 390 395 400
 267 His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly
 268 405 410 415
 270 Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser
 271 420 425 430
 273 Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn
 274 435 440 445
 276 Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ile Ile
 277 450 455 460
 279 Met Leu Gly Lys
 280 465
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 284 <211> LENGTH: 1029
 285 <212> TYPE: DNA
 286 <213> ORGANISM: *Bacillus* sp.
 288 <400> SEQUENCE: 5
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 291 gaggttacag ccatgacaca ttttctatgg ctgaggcgta tagaatccga agcgccaccg 180
 292 ggcaatcgcc tgcttattat ggctgcgatt atgcagagg atggcttcaa acagcaaata 240
 293 ttgaagattc aatagatgta agctgcaacg gcgatttaat gtcttattgg aaaaatggcg 300
 294 gaattccgca aatcgtttt cacctggcgca accctgcatt tcagtcaggg cattttaaaa 360
 295 caccgattac aaatgatcag tataaaaaca tattagattc agcaacagcg gaaggaaagc 420
 296 ggctaaatgc catgctcagc aaaattgcgt acggacttca agagttggag aaccaaggtg 480
 297 tgcctgttct gttcaggccg ctgcatttgc tgaacggcgatggtttgg tggggactca 540
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 300 acgccaaccg agattttaaa actgattttt accccggcgatggtttgg tggggactca 720
 301 gattagatgc gtatttcaa gatgcctact cgatcaatgg atacgatcag ctaacagcg 780
 302 ttaataaacc atttgctttt acagaagtcg gcccggaaac agcaaacggc agtttcgatt 840
 303 acagcctgtt catcaatgca ataaaacaaa aatatcctaa aaccatttac ttctggcat 900
 304 ggaatgatga atggagcgca gcagtaaaca agggtgcattc agctttatcatgacagct 960
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 310 <211> LENGTH: 362
 311 <212> TYPE: PRT
 312 <213> ORGANISM: *Bacillus* sp.
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 319 20 25 30
 321 Asn Pro Asn Ala Gln Gln Thr Thr Lys Thr Val Met Asn Trp Leu Ala
 322 35 40 45
 324 His Leu Pro Asn Arg Thr Glu Asn Arg Val Leu Ser Gly Ala Phe Gly
 325 50 55 60
 327 Gly Tyr Ser His Asp Thr Phe Ser Met Ala Glu Ala Asp Arg Ile Arg

VERIFICATION SUMMARY

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